

A

MUSCLE-N
m MGGQITRNTIHD-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG----

BRAIN-N
m MGNNFSSVSSLQRGNPSRASRG---HPQNLKE-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG---- 55
r MGNNFSSVSSLQRGNPSRASRG---HPQNLKD-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG---- 55
h MGNNFSSVSSLQRGNPSRASRG---HPQNLKD-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG---- 55
d MGLSDIPANYMQGSHPEHLTLHPQQQHONQQLHLQHQMQQLHNAMPTPAQAAQVLAESNELLHMSTKDKLSSKKKMLLKKIKKH FGL 90

NLS1
m -----GGLPATPLLFPHPTKCSQILMDLSHKAVKROASFCNAITFSNRPVLIYEQVRLKITKQCCNSGALRLGFTSKDPSRIHPD 136
r -----GGLPATPLLFPHPTKCSQILMDLSHKAVKROASFCNAITFSNRPVLIYEQVRLKITKQCCNSGALRLGFTSKDPSRIHPD 136
h -----GGLPATPLLFPHPTKCSQILMDLSHKAVKROASFCNAITFSNRPVLIYEQVRLKITKQCCNSGALRLGFTSKDPSRIHPD 136
d VRRSPSSCPGPNNLFPLOFH-SVHCNIRISRDGTLARRFESFCRAITFSARPVIRNERICVKFAEISNNWNGGIRFGFTSKNDP-VTLEG 178

NLS2
m -----GGLPATPLLFPHPTKCSQILMDLSHKAVKROASFCNAITFSNRPVLIYEQVRLKITKQCCNSGALRLGFTSKDPSRIHPD 136
r -----GGLPATPLLFPHPTKCSQILMDLSHKAVKROASFCNAITFSNRPVLIYEQVRLKITKQCCNSGALRLGFTSKDPSRIHPD 136
h -----GGLPATPLLFPHPTKCSQILMDLSHKAVKROASFCNAITFSNRPVLIYEQVRLKITKQCCNSGALRLGFTSKDPSRIHPD 136
d VRRSPSSCPGPNNLFPLOFH-SVHCNIRISRDGTLARRFESFCRAITFSARPVIRNERICVKFAEISNNWNGGIRFGFTSKNDP-VTLEG 178

NHR1
m SLPKYACPDIVSQSCFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPALVLDVYGLTRVQLLDS----- 218
r SLPKYACPDIVSQSCFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPALVLDVYGLTRVQLLDS----- 218
h SLPKYACPDIVSQSCFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPALVLDVYGLTRVQLLDS----- 218
d TLPKYACPDITNRPGFWAKALPEEYCEKDNILYYVNGAGSVIYGINNEEGKVILTIDIRSLGTVIDITGNCTGIEFLDSRIYMYQQQ 268

LRS1 *
m ELVLBDCLRRSFTALRRSLRCEADE-----ARLSVSLCDLNVPGADGDDGAPPAG--CPIPNLSLNSQHSRALP-A 288
r ELVLBDCLRRSFTALRRSLRCEADE-----ARLSVSLCDLNVPGADGDDGAPPAG--CPIPNLSLNSQHSRALP-A 288
h ELVLBDCLRRSFTALRRSLRCEADE-----ARLSVSLCDLNVPGADGDDGAPPAG--CPIPNLSLNSQHSRALP-A 288
d PAATIMATVBAQQQMPOAANASSALNSHHPHQSSRRSLPGHTAIEHLEERHVMPSLQSLHLGNGGGSVASVEAAIAHDLANCLPPL 358

PKB
m QLDG-----DLRFHALRAGAHVRILDEQVARLEHGRDERALVFTSRPVVAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
r QLDG-----DLRFHALRAGAHVRILDEQVARLEHGRDERALVFTSRPVVAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
h QLDG-----DLRFHALRAGAHVRILDEQVARLEHGRDERALVFTSRPVVAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
d RYNANGRLIPVFFHNT-KGRNVRSLQDRFVASRTESDFCQGYVFTARPIRIGKLVQVLTKEQMYVGCALALGLISGNPAMLCNDLIND 447

NHR2
m QLDG-----DLRFHALRAGAHVRILDEQVARLEHGRDERALVFTSRPVVAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
r QLDG-----DLRFHALRAGAHVRILDEQVARLEHGRDERALVFTSRPVVAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
h QLDG-----DLRFHALRAGAHVRILDEQVARLEHGRDERALVFTSRPVVAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
d RYNANGRLIPVFFHNT-KGRNVRSLQDRFVASRTESDFCQGYVFTARPIRIGKLVQVLTKEQMYVGCALALGLISGNPAMLCNDLIND 447

LRS2 *
m PEALVDRKEFWAVCR-VPGPLHSGDILGLVNNADGELHLSHNGAAGMQLCVDAQPLWMLFSLHCAITQVRIIGSTIMTERGGP----- 457
r PEALVDRKEFWAVCR-VPGPLHSGDILGLVNNADGELHLSHNGAAGMQLCVDAQPLWMLFSLHCAITQVRIIGSTIMTERGGP----- 457
h PEALVDRKEFWAVCR-VPGPLHSGDILGLVNNADGELHLSHNGAAGMQLCVDAQPLWMLFSLHCAITQVRIIGSTIMTERGGP----- 457
d SDFLDRPFWVWVSKDIAAAPQRGDEIAFVAPNGEVSISKNNGPAVVVHVVDQLQWAFLDVYGSTQSLRMFRQQLPNMVAYPSQPQV 537

SP1
m ----SLPCSPASTPSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPCLGQWSD--- 519
r ----SLPCSPASTPSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPCLGQWSD--- 519
h ----SLPCSPASTPSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPCLGQWSD--- 519
d NVNASSSSACNAASISRMPLMTESMSLNLNAGATAKLLHPSQLSVAQSTSTLASAGGVNGSRMISMPSNGDILQIQHNGGCTVLVVNLPP 627

SP2
m ----SLPCSPASTPSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPCLGQWSD--- 519
r ----SLPCSPASTPSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPCLGQWSD--- 519
h ----SLPCSPASTPSPSALGIRL-SD-----PLLSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPCLGQWSD--- 519
d NVNASSSSACNAASISRMPLMTESMSLNLNAGATAKLLHPSQLSVAQSTSTLASAGGVNGSRMISMPSNGDILQIQHNGGCTVLVVNLPP 627

RZD
m HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTYRSS 574
r HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTYRSS 574
h HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTYRSS 574
d HMCLCYSCGLRLKKALH-ACCPICRRPIKDIKTYRSS 574

B

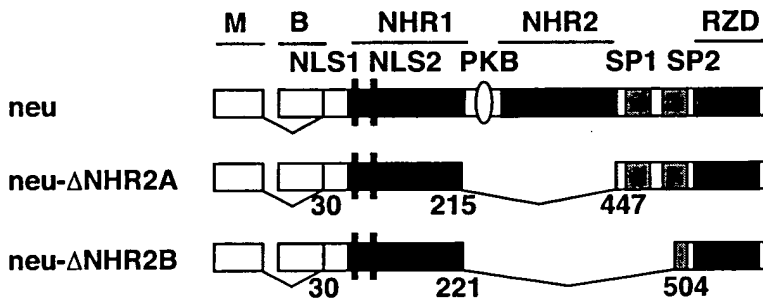
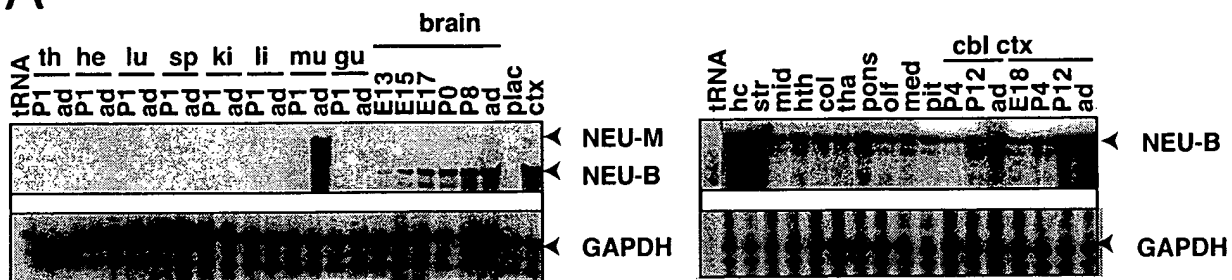


FIGURE 1

A



B

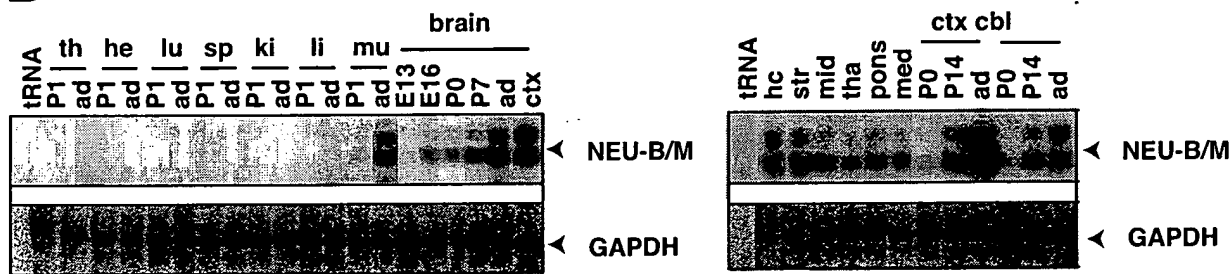


FIGURE 2

0900360 03444

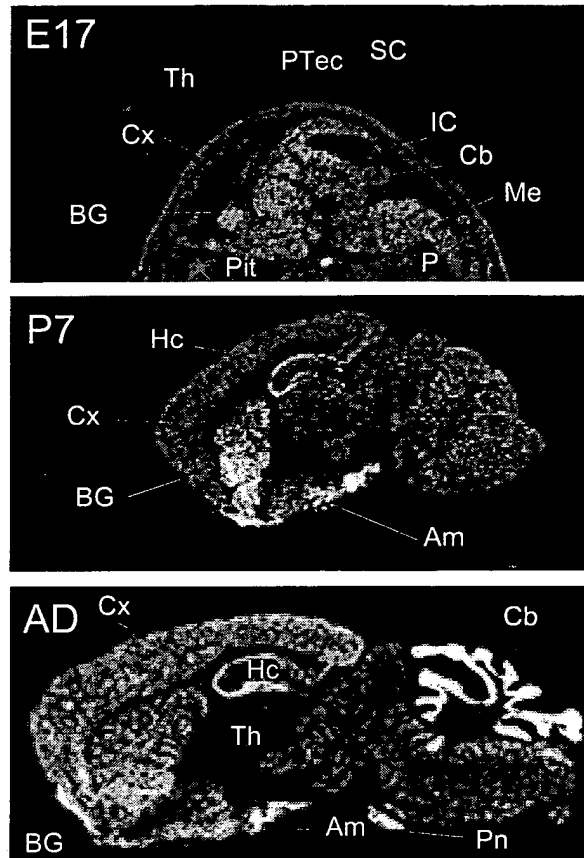


FIGURE 3

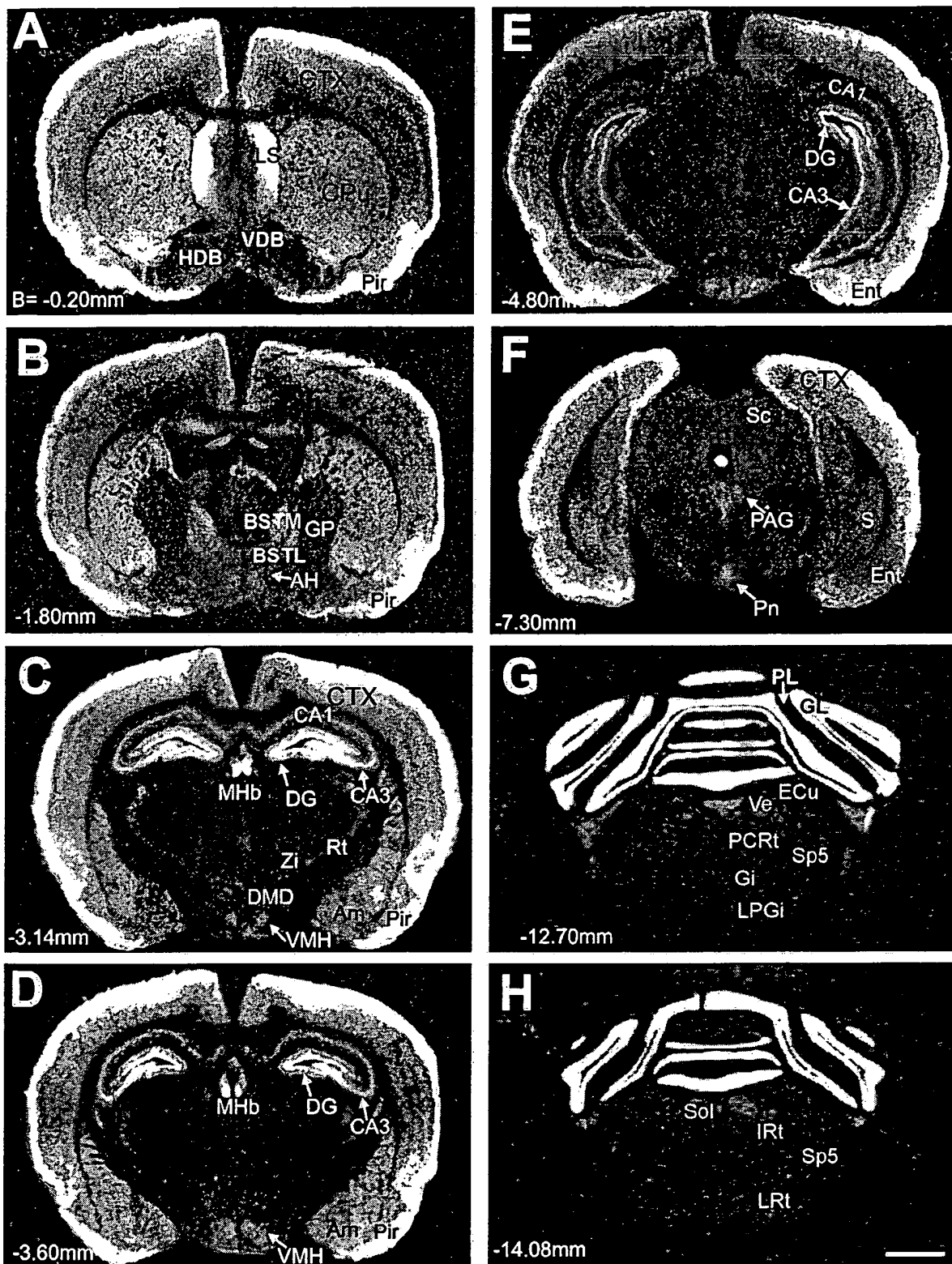


FIGURE 4

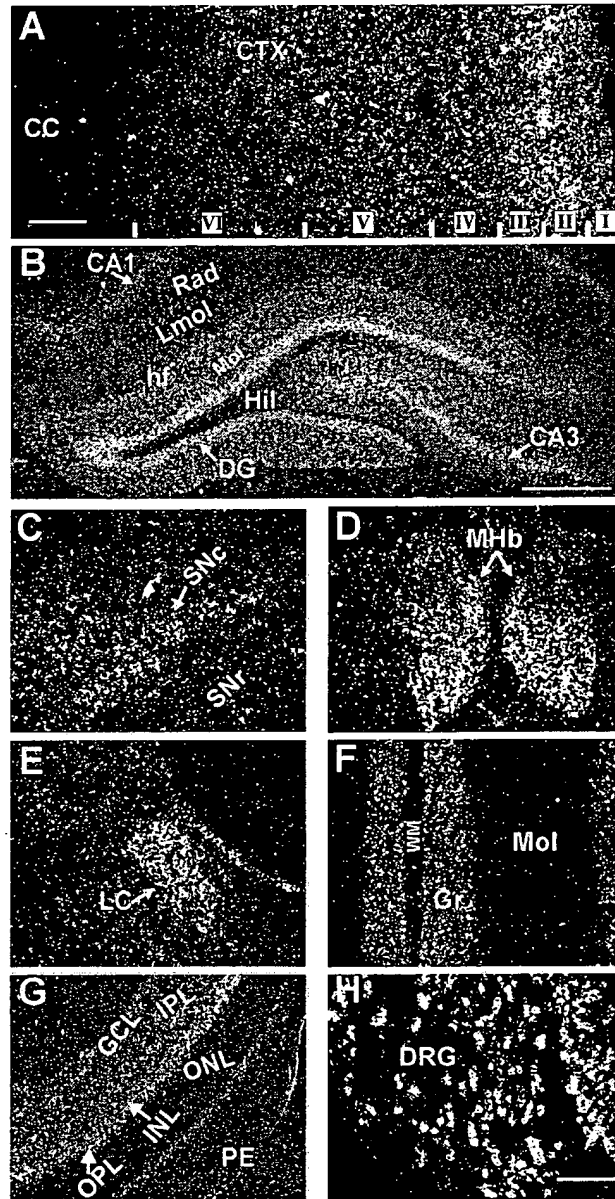


FIGURE 5

Figure 1 consists of 12 micrographs (A-L) showing the distribution of 125 I-tyrosine in various brain regions. The panels are arranged in a 4x3 grid. Panels A-C show CTX, Hil, DG, Mol, Rad, CA3, and Or. Panels D-F show PoDG, LS, and SNc. Panels G-I show GP and Sc. Panels J-L show DRG, GL, and Pi. Arrows in D point to specific cells. Scale bars are present in D, E, and L.

FIGURE 6

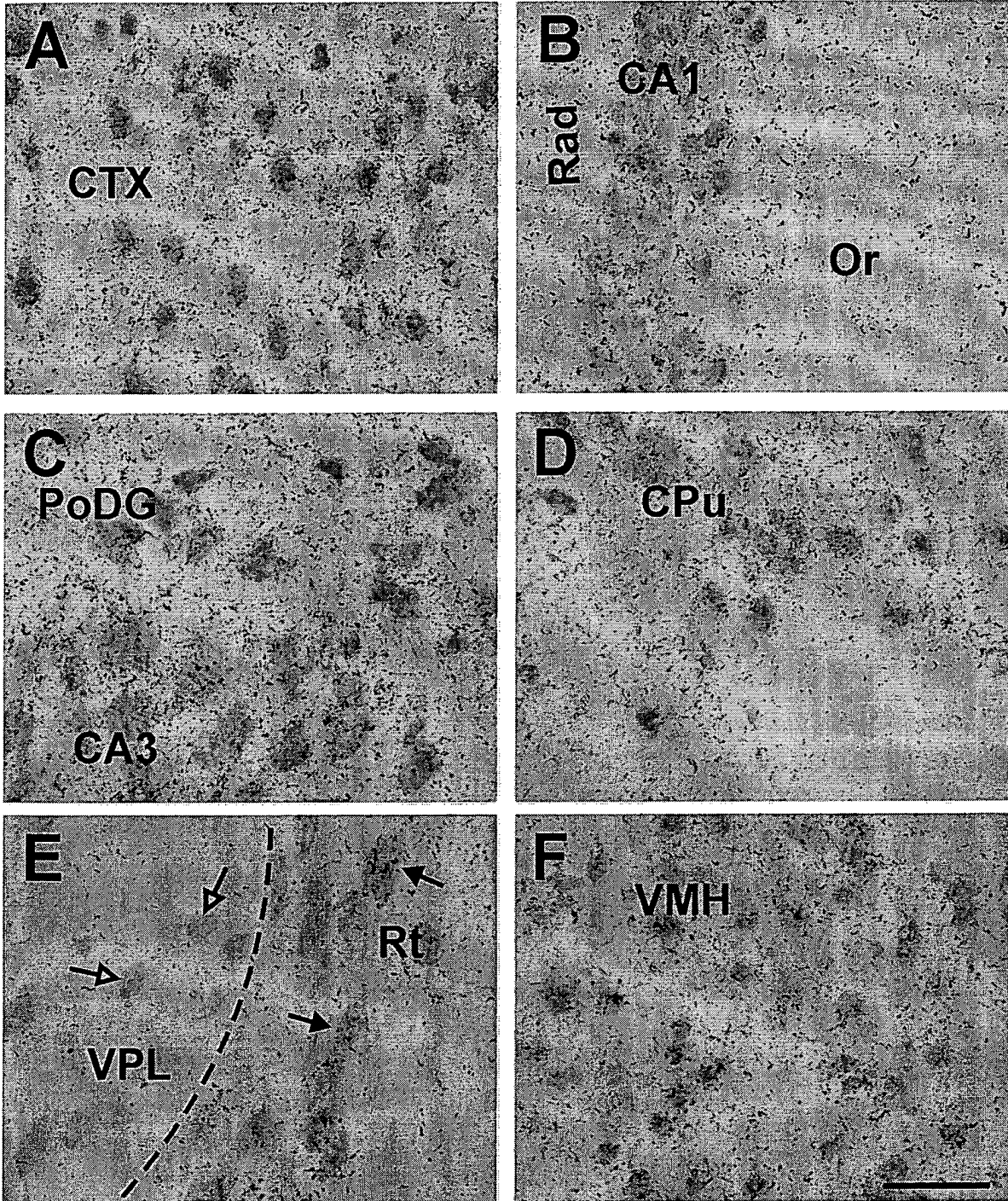


FIGURE 7

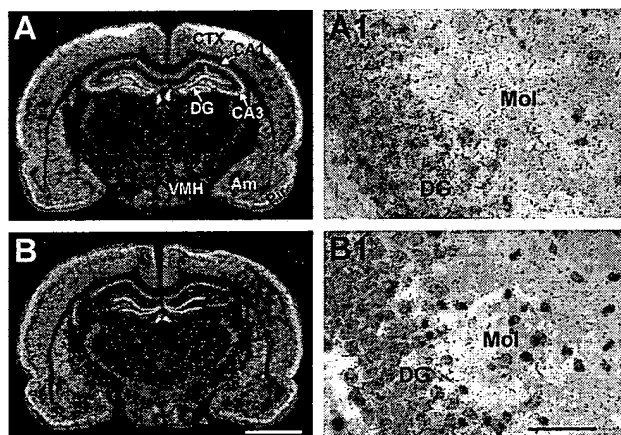


FIGURE 8

bioRxiv preprint doi: <https://doi.org/10.1101/20200320>; this version posted March 20, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

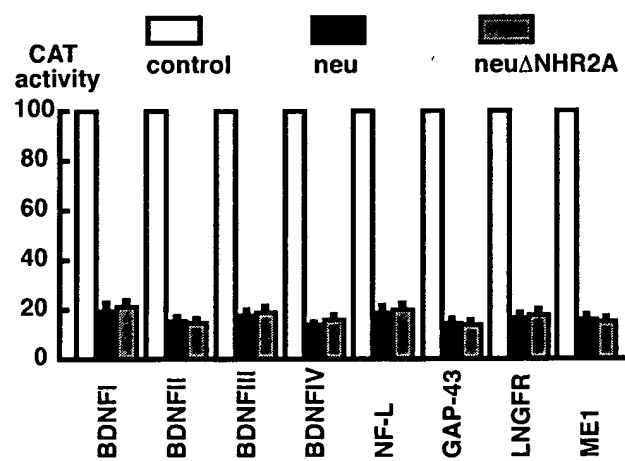


FIGURE 9

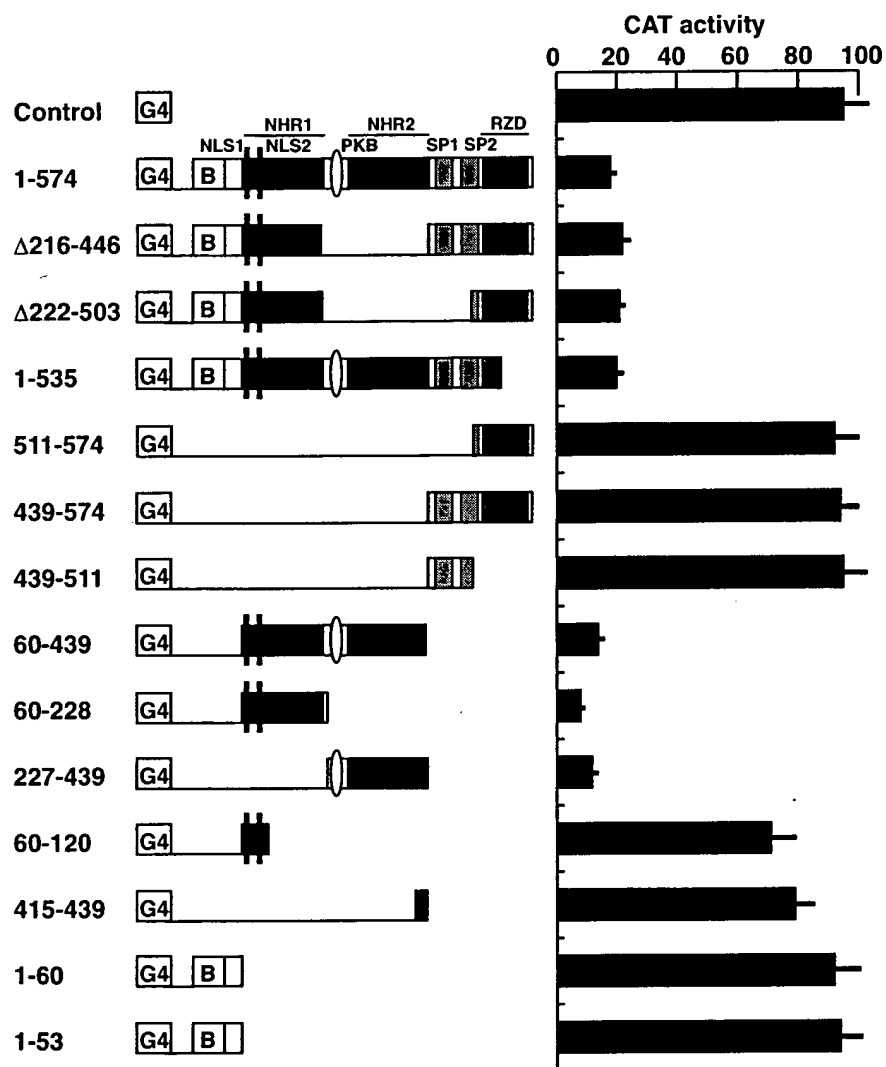


FIGURE 10

Figure 1 consists of eight panels (A-H) showing fluorescence microscopy images of Drosophila ommatidia. Panels A-D show wild-type ommatidia with different numbers of cells (1-574, 1-120, 60-120, 1-60). Panels E-F show ommatidia with 1-574 cells treated with LMB or RA. Panels G-H show ommatidia expressing FLAG or EGFP. Bright spots indicate nuclei.

FIGURE 11

h1I	FHPHTKGSQILMDLSHKAVKR-QASFCNAITFSNRPVLIYEQVRLKITTKKQCCWSGAILRL
h2I	FHAQAKGKNVRLDGHSRRATR-RNSFCNGVTETORPIRLYEQVRLRLVAVRPGWSGAILRF
h3	FHAEAKGAQVRLDTRGCIARR-RTTFHDGIVFSQRPVRLGERVALRVLREESGWCGGLRV
dI	FHS-VHGDNIRISRDGTLARR-FESFCRAITFSARPVRINERICVKFAEISNNWNGGIRF
dII	FHNTK-GRNVRLSQDRFVASRTESDFCQGYVETARPIRIGEKLIVQVLKTEQMYVGALAL
h2II	FHATR-GPDVSLSADRKVACAPRPDGGRTLVESERPRLRPGESLFVEVGRPGLAAPGALAF
h1II	FHALRAGAHVRILDEQTVARVEHGRDERALVELSRPVRVAETIFVKVTRSGGARPGALS
h1I	GETSKDPSRIHPDSLPHYACPDLVSGSGFWAKAL-PEEFANEENITAFWVDKKGRVFHRI
h2I	GETAHDPSSLMSAQDIPKYACPDLVTRPGYFAKAL-PENLALRDTVLAYWADRHCGRVFYSV
h3	GETRLDPACVSVPSLPPFLCPDLEEQSPTWAAVL-PEGCALTGDLVRFWVDRRGCLFAKV
dI	GETSNDEPVTLEG-TLPKYACPDLTNRPGFWAKAL-HEQYCEKDNILYYYVNGAGDVIYGI
dII	GITSCNPAMLQP-NDLPNDSDFLLDRPEYWWVSKDIAAAPQRGDEIAFFVAPNGEVSISK
h2II	GITSCDPGVLRP-NELPADPDALLDRKEYWWVAR-AGPVPSGGDALSFTRLRPGGDVLLGI
h1II	GVTTCDPGLRTP-ADLPFSPEALVDRKEFWAVCR-VPGPLHSGDILGLVFNADGELHLSH
h1I	NDSAVMLFFSGVVRTADPLWALVDVYG-LTRGVQLL
h2I	NDGEPVLFHCGVAVGGPLWALIDVYG-ITDEVQLL
h3	NAGCRLLLRGVVPGAPLWAVMDVYG-TTKAIELL
dI	NNEEKGVILTGIDTRSLLWTVIDIYG-NCTGIEFL
dII	NNGPAVVVMH-VDQSLQLWAFIDVYG-STQSLRMF
h2II	NGRPRGRLLC-VDTTQALWAFFAVRGGVAGQLRLL
h1II	NGAAAGMQLC-VDASQPLWMLFGLHG-TITQIRIL

FIGURE 12

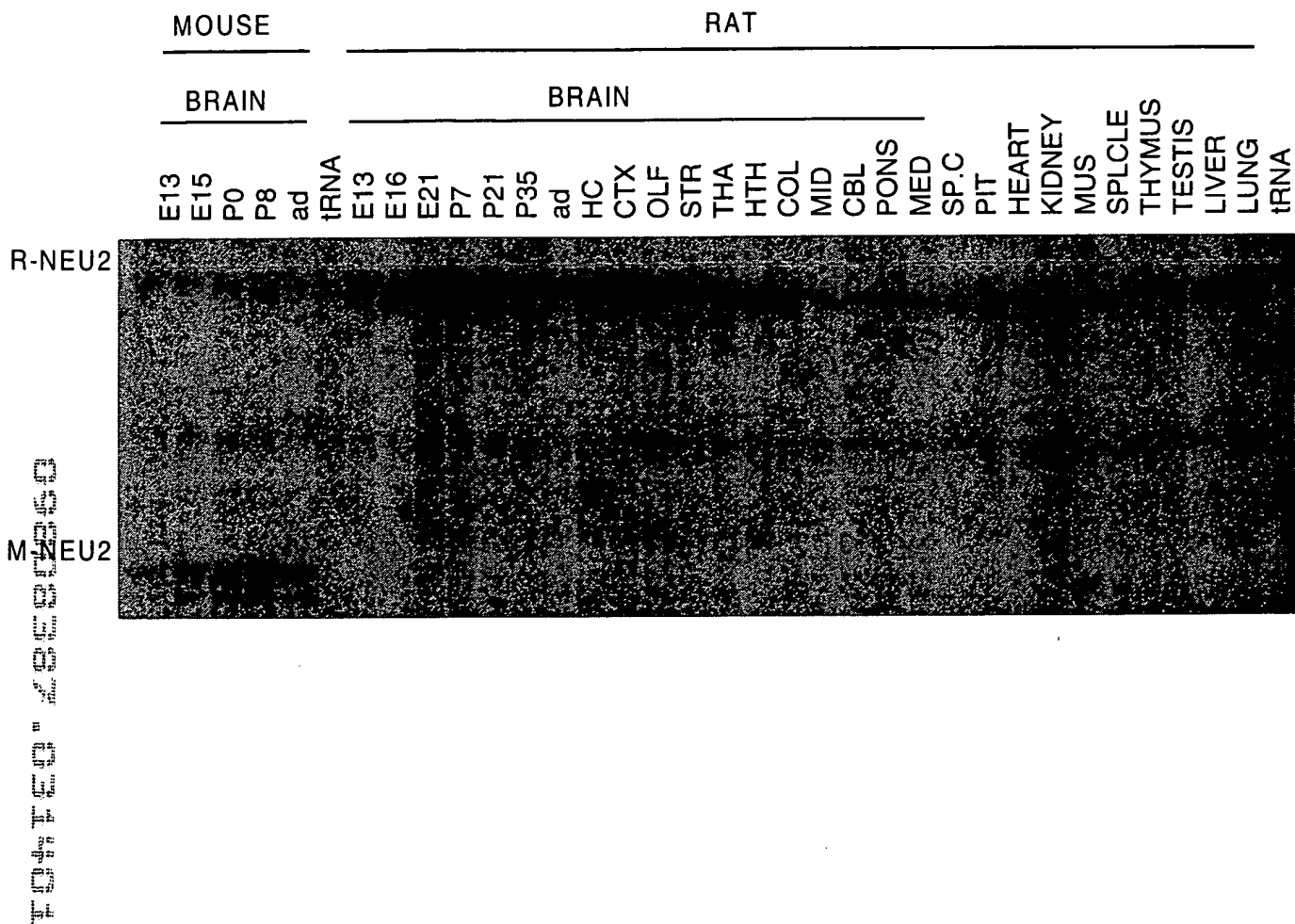


FIGURE 13

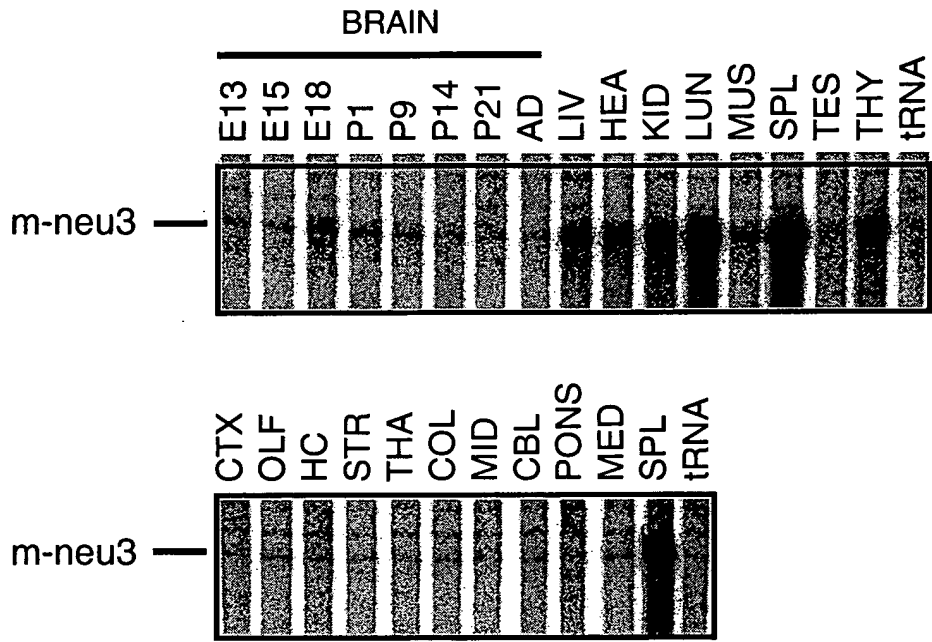


FIGURE 14

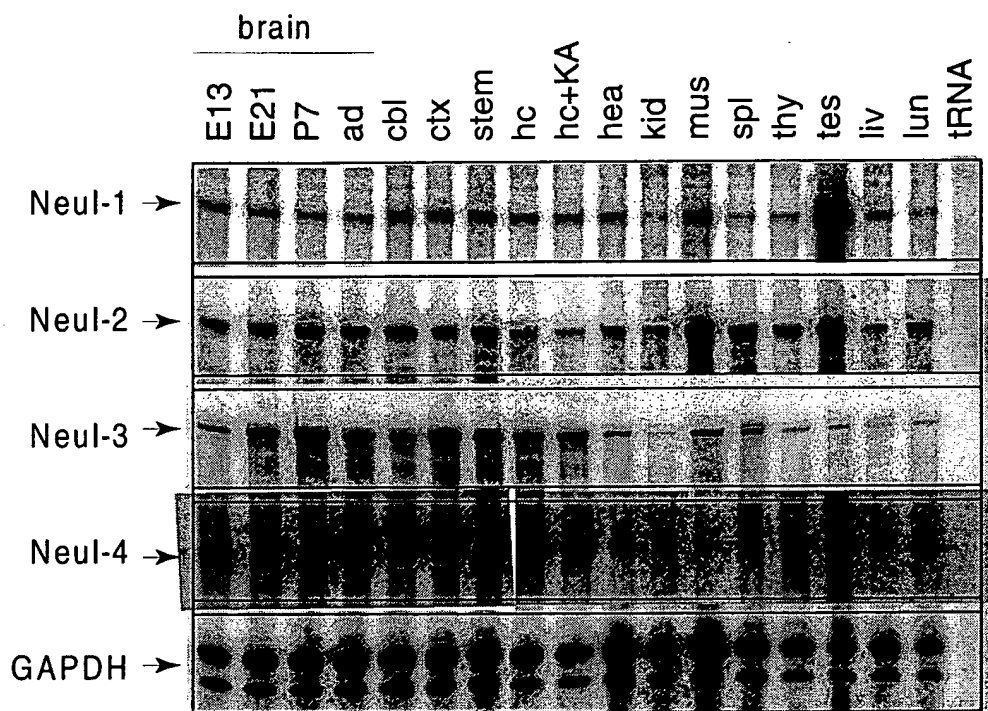


FIGURE 15